

2010-11-01 Substitute Sequence Listing
SEQUENCE LISTING

<110> Feldmann, Kenneth
Pennell, Roger
Kwok, Shing
Dang, Van-Dinh
Zhang, Hongyu

<120> NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR

INCREASING PLANT SIZE AND INCREASING THE NUMBER AND SIZE OF LEAVES

<130> 2750-1573PUS1

<140> 10/572,827

<141> 2006-03-21

<150> PCT/US03/25997

<151> 2003-08-18

<160> 50

<170> PatentIn version 3.0

<210> 1

<211> 1453

<212> DNA

<213> Zea mays subsp. mays

<220>

<221> misc_feature

<222> (1)..(1453)

<223> ceres Seq. ID no. 12355477

<400> 1

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caagaattgt tgcacgcgat aaaggctcgg tgaaaataca agcaaatacct gggaactcgc 420
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 gatgactgtc ctaaaaggag gcagtaagat gatgggacat gtcttacgaa attttcagct 1140
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<210> 2
 <211> 576
 <212> DNA
 <213> Zea mays subsp. mays

<400> 2
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<210> 3
 <211> 192
 <212> PRT
 <213> Zea mays subsp. mays

<220>
 <221> peptide
 <222> (1)..(192)
 <223> ceres Seq. ID no. 12355478

<400> 3

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 20 25 30
 Gly Trp Thr Asp Glu Arg His Arg Leu Tyr Ile Ser Ser Met Glu Ala
 35 40 45
 Ser Phe Val Asp Gln Leu Tyr Asn His Gly Ser Arg Pro Arg Asn Ala
 50 55 60
 Asn Gly Thr Ala Phe Lys Ala Leu Arg Arg Glu Tyr Val Glu Tyr Glu
 65 70 75 80
 Lys Thr Asp Ala Pro Val Arg Arg Gly Ala Lys Cys Cys Gly Val Pro
 85 90 95
 Ala Asn Pro Trp Met Gln His Phe Arg Pro Arg Ser Asp Gly Gly Asn
 100 105 110
 Asn Ala Arg Gly Asp Gly Leu Gly Asp Ser Val Gly Asp Leu Glu Ser
 115 120 125
 Gly Thr Glu Ala Asn Arg Lys Ser Leu Ser Ala Ser His Gly Arg Glu
 130 135 140
 Arg Asp Ala Cys Glu Gly Glu Pro Gln Leu Leu His Glu Ser Arg Glu
 145 150 155 160
 Val Ser Asp Gln Asn Phe Ala Asp Asp Glu Ala Glu Ala Glu Thr Glu
 165 170 175
 Ser Met Lys Ala Tyr Lys Lys Arg Arg Leu Ser Arg Thr Met Ile Asn
 180 185 190

<210> 4
 <211> 489
 <212> DNA
 <213> Zea mays subsp. mays

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 aaggctctcc gcagggagta cgtcgagtat gagaagaccg atgctcctgt gcgaaggggg 180
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 ggagaacccc agcttctcca tgaaagtaga gaggtctctg atcaaaattt tgctgacgac 420
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 atgatcaac 489

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<210> 5
 <211> 163
 <212> PRT
 <213> Zea mays subsp. mays

<220>
 <221> peptide
 <222> (1)..(163)
 <223> ceres Seq. ID no. 12355479

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 20 25 30
 Arg Asn Ala Asn Gly Thr Ala Phe Lys Ala Leu Arg Arg Glu Tyr Val
 35 40 45
 Glu Tyr Glu Lys Thr Asp Ala Pro Val Arg Arg Gly Ala Lys Cys Cys
 50 55 60
 Gly Val Pro Ala Asn Pro Trp Met Gln His Phe Arg Pro Arg Ser Asp
 65 70 75 80
 Gly Gly Asn Asn Ala Arg Gly Asp Gly Leu Gly Asp Ser Val Gly Asp
 85 90 95
 Leu Glu Ser Gly Thr Glu Ala Asn Arg Lys Ser Leu Ser Ala Ser His
 100 105 110
 Gly Arg Glu Arg Asp Ala Cys Glu Gly Glu Pro Gln Leu Leu His Glu
 115 120 125
 Ser Arg Glu Val Ser Asp Gln Asn Phe Ala Asp Asp Glu Ala Glu Ala
 130 135 140
 Glu Thr Glu Ser Met Lys Ala Tyr Lys Lys Arg Arg Leu Ser Arg Thr
 145 150 155 160
 Met Ile Asn

<210> 6
 <211> 441
 <212> DNA
 <213> Zea mays subsp. mays

<400> 6
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 gtgcgaaggg gggctaagtg ctgcggcggt cctgcaaadc cttggatgca gcatttcagg 180
 ccacgtagtg atggcggtaa taacgcgcga ggcgatgggc tcggggattc tgtgggcgat 240
 cttgaatctg gcactgaggc aaaccggaag agcctctcag cgtctcatgg aagggaacgg 300
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<210> 7
<211> 147
<212> PRT
<213> Zea mays subsp. mays

<220>
<221> peptide
<222> (1)..(147)
<223> ceres Seq. ID no. 12355480

<400> 7
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20 25 30
Glu Tyr Glu Lys Thr Asp Ala Pro Val Arg Arg Gly Ala Lys Cys Cys
35 40 45
Gly Val Pro Ala Asn Pro Trp Met Gln His Phe Arg Pro Arg Ser Asp
50 55 60
Gly Gly Asn Asn Ala Arg Gly Asp Gly Leu Gly Asp Ser Val Gly Asp
65 70 75 80
Leu Glu Ser Gly Thr Glu Ala Asn Arg Lys Ser Leu Ser Ala Ser His
85 90 95
Gly Arg Glu Arg Asp Ala Cys Glu Gly Glu Pro Gln Leu Leu His Glu
100 105 110
Ser Arg Glu Val Ser Asp Gln Asn Phe Ala Asp Asp Glu Ala Glu Ala
115 120 125
Glu Thr Glu Ser Met Lys Ala Tyr Lys Lys Arg Arg Leu Ser Arg Thr
130 135 140
Met Ile Asn
145

<210> 8
<211> 1494
<212> DNA
<213> Zea mays subsp. mays

<220>
<221> misc_feature
<222> (1)..(1494)
<223> ceres Seq. ID no. 12410516

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<400> 8

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tcgggcgaaa tacacgcaa tccttggaat tttgcatccc tttgctggct cttttctgat 540
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ggtggcattg ccaagggaaa ccgagtcttg gacacgatgt ccgccgggtg gacggacgag 660
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gagtacatcg agtatgagaa gaccagtgcc cctgtgcgaa gtggggctaa atgctgcgtc 840
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gacgcggtcg aggcctcagt gggcgaccat gagtcgggta ctcaggcaag ccgcaagagc 960
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<210> 9

<211> 585

<212> DNA

<213> Zea mays subsp. mays

<400> 9

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| tatataagct ccatggaggc ttctttttgtc gatcagctat acaacccatgg aaacccatccg | 180 |
| cacgacgcaa atggcgctgg cttcaagggt ctccgcaggg ggggtgtggga gtacatcgag | 240 |
| tatgagaaga ccagtgccccc tgtgcgaagt ggggctaaat gctgcgtccc tgcaaatcct | 300 |
| tggatccggc atttcaggcc acgtgactgc ggtagtaacg cacagagtga cgcggtcgag | 360 |
| gcctcagtgg gcgaccatga gtcgggtact caggcaagcc gcaagagccc ttcagtgtct | 420 |
| catggaaggg aacgggggagc ttgtaagggga gaaccccaga ttctacatga aagtacagag | 480 |
| gtctctgatc aaaattttgtc tgacgatgag gctgaagctg aaacagaatc aatgaaagca | 540 |
| tgcaagaaaa ggagactaag cagggtcttg cactccgggtg ctgaa | 585 |

<210> 10
 <211> 195
 <212> PRT
 <213> Zea mays subsp. mays

 <220>
 <221> peptide
 <222> (1)..(195)
 <223> ceres Seq. ID no. 12410517

<400> 10
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 20 25 30
 Trp Thr Asp Glu Arg His Met Leu Tyr Ile Ser Ser Met Glu Ala Ser
 35 40 45
 Phe Val Asp Gln Leu Tyr Asn His Gly Asn His Pro His Asp Ala Asn
 50 55 60
 Gly Ala Gly Phe Lys Val Leu Arg Arg Gly Val Trp Glu Tyr Ile Glu
 65 70 75 80
 Tyr Glu Lys Thr Ser Ala Pro Val Arg Ser Gly Ala Lys Cys Cys Val
 85 90 95
 Pro Ala Asn Pro Trp Ile Arg His Phe Arg Pro Arg Asp Cys Gly Ser
 100 105 110
 Asn Ala Gln Ser Asp Ala Val Glu Ala Ser Val Gly Asp His Glu Ser
 115 120 125
 Gly Thr Gln Ala Ser Arg Lys Ser Pro Ser Val Ser His Gly Arg Glu
 130 135 140
 Arg Gly Ala Cys Lys Gly Glu Pro Gln Ile Leu His Glu Ser Thr Glu
 145 150 155 160
 Val Ser Asp Gln Asn Phe Ala Asp Asp Glu Ala Glu Ala Glu Thr Glu
 165 170 175

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Ser Met Lys Ala Cys Lys Lys Arg Arg Leu Ser Arg Ala Leu His Ser
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Gly Ala Glu
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<210> 11
<211> 501
<212> DNA
<213> Zea mays subsp. mays

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cgaagtgggg ctaaattgctg cgtcccctgca aatccttgga tccggcattt caggccacgt 240
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ggtactcagg caagccgcaa gagcccttca gtgtctcatg gaagggaacg gggagcttgt 360
aaggggagaac cccagattct acatgaaagt acagaggtct ctgatcaaaa ttttgctgac 420
gatgaggctg aagctgaaac agaatacatg aaagcatgca agaaaaggag actaagcagg 480
gctttgcact ccggtgctga a 501

<210> 12
<211> 167
<212> PRT
<213> Zea mays subsp. mays

<220>
<221> peptide
<222> (1)..(167)
<223> ceres Seq. ID no. 12410518

<400> 12
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1 5 10 15
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20 25 30
His Asp Ala Asn Gly Ala Gly Phe Lys Val Leu Arg Arg Gly Val Trp
35 40 45
Glu Tyr Ile Glu Tyr Glu Lys Thr Ser Ala Pro Val Arg Ser Gly Ala
50 55 60
Lys Cys Cys Val Pro Ala Asn Pro Trp Ile Arg His Phe Arg Pro Arg
65 70 75 80
Asp Cys Gly Ser Asn Ala Gln Ser Asp Ala Val Glu Ala Ser Val Gly
85 90 95

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Asp His Glu Ser Gly Thr Gln Ala Ser Arg Lys Ser Pro Ser Val Ser
 100 105 110
 His Gly Arg Glu Arg Gly Ala Cys Lys Gly Glu Pro Gln Ile Leu His
 115 120 125
 Glu Ser Thr Glu Val Ser Asp Gln Asn Phe Ala Asp Asp Glu Ala Glu
 130 135 140
 Ala Glu Thr Glu Ser Met Lys Ala Cys Lys Lys Arg Arg Leu Ser Arg
 145 150 155 160
 Ala Leu His Ser Gly Ala Glu
 165

<210> 13
 <211> 471
 <212> DNA
 <213> Zea mays subsp. mays

<400> 13
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 atcgagtatg agaagaccag tgcccctgtg cgaagtgggg ctaaagtctg cgtccctgca 180
 aatccttggg tccggcattt caggccacgt gactgcggta gtaacgcaca gagtgcgcg 240
 gtcgaggcct cagtgggcga ccatgagtcg ggtactcagg caagccgcaa gagcccttca 300
 gtgtctcatg gaagggaacg gggagcttgt aaggggagaac cccagattct acatgaaagt 360
 acagaggctc ctgatcaaaa ttttctgac gatgaggctg aagctgaaac agaatcaatg 420
 aaagcatgca agaaaaggag actaagcagg gctttgcact ccggtgctga a 471

<210> 14
 <211> 157
 <212> PRT
 <213> Zea mays subsp. mays

<220>
 <221> peptide
 <222> (1)..(157)
 <223> ceres Seq. ID no. 12410519

<400> 14
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 20 25 30
 Leu Arg Arg Gly Val Trp Glu Tyr Ile Glu Tyr Glu Lys Thr Ser Ala
 35 40 45
 Pro Val Arg Ser Gly Ala Lys Cys Cys Val Pro Ala Asn Pro Trp Ile
 50 55 60

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Arg His Phe Arg Pro Arg Asp Cys Gly Ser Asn Ala Gln Ser Asp Ala
65 70 75 80
Val Glu Ala Ser Val Gly Asp His Glu Ser Gly Thr Gln Ala Ser Arg
85 90 95
Lys Ser Pro Ser Val Ser His Gly Arg Glu Arg Gly Ala Cys Lys Gly
100 105 110
Glu Pro Gln Ile Leu His Glu Ser Thr Glu Val Ser Asp Gln Asn Phe
115 120 125
Ala Asp Asp Glu Ala Glu Ala Glu Thr Glu Ser Met Lys Ala Cys Lys
130 135 140
Lys Arg Arg Leu Ser Arg Ala Leu His Ser Gly Ala Glu
145 150 155

<210> 15
<211> 409
<212> DNA
<213> Brassica napus
<220>
<221> misc_feature
<222> (1)..(409)
<223> ceres Seq. ID no. 4788142

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gaatgaagat acgcctacag aatggaccga tgagaagcat agtttgatc ttaaataaat 240
ggaagcttcc ttcgttgatc agctgtacaa ctccctcggg gcgctcggct ccaaaaacaa 300
caaggatact gtcggaccat cgagaagggt cggtgatggg ggaaaacctt ctgaagaaca 360
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<210> 16
<211> 276
<212> DNA
<213> Brassica napus

<400> 16
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gatgagaagc atagtttgta tcttaaatca atggaagctt ctttcgttga tcagctgtac 180
aactccctcg gtgcgctcgg ctccaaaaac aacaaggata ctgtcggacc atcgagaagg 240
ttcgggtgatg gtggaaaacc ttctgaagaa caggta 276

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<210> 17
 <211> 92
 <212> PRT
 <213> Brassica napus
 <220>
 <221> peptide
 <222> (1)..(92)
 <223> ceres Seq. ID no. 4788143

<400> 17
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 1 5 10 15
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 20 25 30
 Glu Asp Thr Pro Thr Glu Trp Thr Asp Glu Lys His Ser Leu Tyr Leu
 35 40 45
 Lys Ser Met Glu Ala Ser Phe Val Asp Gln Leu Tyr Asn Ser Leu Gly
 50 55 60
 Ala Leu Gly Ser Lys Asn Asn Lys Asp Thr Val Gly Pro Ser Arg Arg
 65 70 75 80
 Phe Gly Asp Gly Gly Lys Pro Ser Glu Glu Gln Val
 85 90

<210> 18
 <211> 198
 <212> DNA
 <213> Brassica napus

<400> 18
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 ggctccaaaa acaacaagga tactgtcgga ccatcgagaa gggtcggtga tgggtggaaaa 180
 ccttctgaag aacaggta 198

<210> 19
 <211> 66
 <212> PRT
 <213> Brassica napus
 <220>
 <221> peptide
 <222> (1)..(66)
 <223> ceres Seq. ID no. 4788144

<400> 19
 Met Tyr Ser Ala Arg Asn Glu Asp Thr Pro Thr Glu Trp Thr Asp Glu
 1 5 10 15

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Lys His Ser Leu Tyr Leu Lys Ser Met Glu Ala Ser Phe Val Asp Gln
 20 25 30
 Leu Tyr Asn Ser Leu Gly Ala Leu Gly Ser Lys Asn Asn Lys Asp Thr
 35 40 45
 Val Gly Pro Ser Arg Arg Phe Gly Asp Gly Gly Lys Pro Ser Glu Glu
 50 55 60
 Gln Val
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<210> 20
 <211> 186
 <212> DNA
 <213> Brassica napus

<400> 20
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 tatgaa 186

<210> 21
 <211> 62
 <212> PRT
 <213> Brassica napus

<220>
 <221> peptide
 <222> (1)..(62)
 <223> ceres Seq. ID no. 4788145

<400> 21
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 20 25 30
 Val Arg Ser Ala Pro Lys Thr Thr Arg Ile Leu Ser Asp His Arg Glu
 35 40 45
 Gly Ser Val Met Val Glu Asn Leu Leu Lys Asn Arg Tyr Glu
 50 55 60

<210> 22
 <211> 486
 <212> DNA
 <213> Brassica napus

<220>
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 <222> (1)..(486)

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<223> ceres Seq. ID no. 4796909

<400> 22

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gcgaggaatg aagatacgcc tacagaatgg accgatgaga agcatagttt gtatcttaaa 240
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gaacagaaga tgaatgtgag gcagcctgag tatcgtctca atggaagaca cggtcgtcgc 420
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<210> 23

<211> 393

<212> DNA

<213> Brassica napus

<400> 23

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gatgagaagc atagtittgta tcttaaatca atggaagctt ccttcggtga tcagctgtac 180
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ttcgggtgatg gtggaaaacc ttctgaagaa cagaagatga atgtgaggca gcctgagtat 300
cgtctcaatg gaagacacgg tcgtcgtctt cagcagtttc ttaggagtcc atggatcaag 360
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<210> 24

<211> 131

<212> PRT

<213> Brassica napus

<220>

<221> peptide

<222> (1)..(131)

<223> ceres Seq. ID no. 4796910

<400> 24

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Ser Ser Val Gly Glu Glu Thr Thr Ser Ser Met Tyr Ser Ala Arg Asn
          20          25          30

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2010-11-01 Substitute Sequence Listing

Glu Asp Thr Pro Thr Glu Trp Thr Asp Glu Lys His Ser Leu Tyr Leu
35 40 45
Lys Ser Met Glu Ala Ser Phe Val Asp Gln Leu Tyr Asn Ser Leu Gly
50 55 60
Ala Leu Gly Ser Lys Asn Asn Lys Asp Thr Val Gly Pro Ser Arg Arg
65 70 75 80
Phe Gly Asp Gly Gly Lys Pro Ser Glu Glu Gln Lys Met Asn Val Arg
85 90 95
Gln Pro Glu Tyr Arg Leu Asn Gly Arg His Gly Arg Arg Ser His Glu
100 105 110
Phe Leu Arg Ser Pro Trp Ile Lys His Tyr Lys Pro Ser Pro Lys Ser
115 120 125
Leu Thr Asp
130

<210> 25
<211> 315
<212> DNA
<213> Brassica napus

<400> 25
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ggctccaaaa acaacaagga tactgtcgga ccatcgagaa gggtcggtga tggtaggaaa 180
ccttctgaag aacagaagat gaatgtgagg cagcctgagt atcgtctcaa tggaagacac 240
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aagtccttaa cagat 315

<210> 26
<211> 105
<212> PRT
<213> Brassica napus

<220>
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<222> (1)..(105)
<223> ceres Seq. ID no. 4796911

<400> 26
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1 5 10 15
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20 25 30
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35 40 45
Val Gly Pro Ser Arg Arg Phe Gly Asp Gly Gly Lys Pro Ser Glu Glu

2010-11-01 Substitute Sequence Listing

50

55

60

Gln Lys Met Asn Val Arg Gln Pro Glu Tyr Arg Leu Asn Gly Arg His
65 70 75 80

Gly Arg Arg Ser His Glu Phe Leu Arg Ser Pro Trp Ile Lys His Tyr
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Lys Pro Ser Pro Lys Ser Leu Thr Asp
100 105

<210> 27
<211> 243
<212> DNA
<213> Brassica napus

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cagaagatga atgtgaggca gcctgagtat cgtctcaatg gaagacacgg tcgtcgctct 180
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gat 243

<210> 28
<211> 81
<212> PRT
<213> Brassica napus

<220>
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<222> (1)..(81)
<223> ceres Seq. ID no. 4796912

<400> 28
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1 5 10 15
Gly Ser Lys Asn Asn Lys Asp Thr Val Gly Pro Ser Arg Arg Phe Gly
20 25 30
Asp Gly Gly Lys Pro Ser Glu Glu Gln Lys Met Asn Val Arg Gln Pro
35 40 45
Glu Tyr Arg Leu Asn Gly Arg His Gly Arg Arg Ser His Glu Phe Leu
50 55 60
Arg Ser Pro Trp Ile Lys His Tyr Lys Pro Ser Pro Lys Ser Leu Thr
65 70 75 80
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2010-11-01 Substitute Sequence Listing

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 <211> 1014
 <212> DNA
 <213> Arabidopsis thaliana
 <220>
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 <222> (1)..(1014)
 <223> ceres Seq. ID no. 12321174

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 tgatcagttt accgtcctac aaaatggttg ctggcagaag gtttaactttg gaaagaaaca 480
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 agagaaggga gaggtgagca aaaaacgaga aagagaagca aataacgatg atagttcatt 720
 gaaggaggat caggttgtgc cggtaaggat ggtgaagccc agaacgtgaa agcattagga 780
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 tccaatggga tatggaaata ggattgggtg ttgttttcgt taaattttgt ctaatgttaa 960
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<210> 30
 <211> 654
 <212> DNA
 <213> Arabidopsis thaliana

<400> 30
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 gctgagacct ctggttctga tgctgattcc aaactggatg aatgtactgc ttggacgaat 180
 gagaaacaca actcatatct tgattattta gagagctcgt ttgttaggca attatactcc 240
 ttgcttggag gtgggactca gagactttct agaactcgtg atgtgcagtc taactctcat 300

2010-11-01 Substitute Sequence Listing

| | |
|---|-----|
| aaatcagctg atcagtttac cgtcctacaa aatgggtgct ggcagaaggt taactttgga | 360 |
| aagaaacaat cttgttttga gacttcatct gagtttcgtt ttcacagaaa ttcattgaga | 420 |
| aataagcctg aaaattccaa cggaaattac accatgggaa ctactgtcca aggagatgtg | 480 |
| ttatgtcatg acgaaaccaa acactcagag gcgtcagggc agaatttcag agaagaagaa | 540 |
| gaagaagaag agaagggaga ggtgagcaaa aaacgagaaa gagaagcaaa taacgatgat | 600 |
| agttcattga aggaggatca ggttgtgccg gtaaggatgg tgaagcccag aacg | 654 |

<210> 31
 <211> 218
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> peptide
 <222> (1)..(218)
 <223> ceres Seq. ID no. 12321175

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 Asp Val Ser Glu Ala Ser Ala Glu Ser Gln Ser Glu Ser Thr Leu Ser
 20 25 30
 Asn Ser Leu Asp Ser Gly Val Thr Ala Glu Thr Ser Arg Ser Asp Ala
 35 40 45
 Asp Ser Lys Leu Asp Glu Cys Thr Ala Trp Thr Asn Glu Lys His Asn
 50 55 60
 Ser Tyr Leu Asp Tyr Leu Glu Ser Ser Phe Val Arg Gln Leu Tyr Ser
 65 70 75 80
 Leu Leu Gly Gly Gly Thr Gln Arg Leu Ser Arg Thr Arg Asp Val Gln
 85 90 95
 Ser Asn Ser His Lys Ser Ala Asp Gln Phe Thr Val Leu Gln Asn Gly
 100 105 110
 Cys Trp Gln Lys Val Asn Phe Gly Lys Lys Gln Ser Cys Leu Glu Thr
 115 120 125
 Ser Ser Glu Phe Arg Phe His Arg Asn Ser Leu Arg Asn Lys Pro Glu
 130 135 140
 Asn Ser Asn Gly Asn Tyr Thr Met Gly Thr Thr Val Gln Gly Asp Val
 145 150 155 160
 Leu Cys His Asp Glu Thr Lys His Ser Glu Ala Ser Gly Gln Asn Phe
 165 170 175
 Arg Glu Glu Glu Glu Glu Glu Lys Gly Glu Val Ser Lys Lys Arg
 180 185 190
 Glu Arg Glu Ala Asn Asn Asp Asp Ser Ser Leu Lys Glu Asp Gln Val

2010-11-01 Substitute Sequence Listing

195

200

205

Val Pro Val Arg Met Val Lys Pro Arg Thr
210 215

<210> 32
<211> 1027
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1027)
<223> ceres Seq. ID no. 12323601

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gtctcaagaa cagttcaagg ttcttcatga tggtttctgg cagaagatta atgtgaaaca 420
acctgaacat cggattaacg gaaggcacgg tggtaattct catgagtttc ttaggagtcc 480
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agaggatatc gatcagaact ttgttaacga aggaataaaa ggcgaaaacg gaagctcgaa 720
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tactatcctt agttacaagt ttcttcatca tatatcccta actataaata tatttatatg 960
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<210> 33
<211> 819
<212> DNA
<213> Arabidopsis thaliana

<400> 33
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2010-11-01 Substitute Sequence Listing

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| tcttccatgt actctgcggg gaaagagtat atggaaacag aatggactaa tgagaagcat | 240 |
| agtttatatc ttaaattctat ggaagcttca ttcgtagatc agttatataa ctcgctcggg | 300 |
| gctctcggga agaacgagaa tgtatccgaa tcaacgaggt tcggtagcgg tagaaaaccg | 360 |
| tctcaagaac agttcaaggt tcttcatgat ggtttctggc agaagattaa tgtgaaacaa | 420 |
| cctgaacatc ggattaacgg aaggcacggt ggtaattctc atgagtttct taggagtcca | 480 |
| tggtattaagc attataaacc tttagtaaag acacaaatcc cggtaacgga tgagcccgaa | 540 |
| aatcaagttg ttagcagctc taatgggaag aagggaatat gcagctctgg ctcagcctct | 600 |
| agtctcaagc agctaagctc tcattcgcgt gaccacgacc aaatcagcgt tggagaagca | 660 |
| gaggtatcgg atcagaactt tgtaacgaa ggaataaaaag gcgaaaacgg aagctcgaag | 720 |
| aagatgaaga cggtgatgat gagtgaatcg tcgagtaccg atcaggttgt tccactcaat | 780 |
| aagctcttgc aacatgacgt aaatttgaag tctgtttct | 819 |

<210> 34

<211> 273

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> peptide

<222> (1)..(273)

<223> ceres Seq. ID no. 12323602

<400> 34

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| Phe Ser Leu Ser Leu His Lys Asp Lys Pro Thr Met Val Gly Asp Tyr | 20 | 25 | 30 | |
| Arg Gly Arg Phe Ser Ser Arg Arg Phe Ser Asp Asp Ser Asp Asp Ser | 35 | 40 | 45 | |
| Ser Asp Asp Ala Ser Ser Val Glu Gly Glu Thr Thr Ser Ser Met Tyr | 50 | 55 | 60 | |
| Ser Ala Gly Lys Glu Tyr Met Glu Thr Glu Trp Thr Asn Glu Lys His | 65 | 70 | 75 | 80 |
| Ser Leu Tyr Leu Lys Ser Met Glu Ala Ser Phe Val Asp Gln Leu Tyr | 85 | 90 | 95 | |
| Asn Ser Leu Gly Ala Leu Gly Lys Asn Glu Asn Val Ser Glu Ser Thr | 100 | 105 | 110 | |
| Arg Phe Gly Ser Gly Arg Lys Pro Ser Gln Glu Gln Phe Lys Val Leu | 115 | 120 | 125 | |
| His Asp Gly Phe Trp Gln Lys Ile Asn Val Lys Gln Pro Glu His Arg | | | | |

2010-11-01 Substitute Sequence Listing

130

135

140

Ile Asn Gly Arg His Gly Gly Asn Ser His Glu Phe Leu Arg Ser Pro
 145 150 155 160
 Trp Ile Lys His Tyr Lys Pro Leu Val Lys Thr Gln Ile Pro Val Thr
 165 170 175
 Asp Glu Pro Glu Asn Gln Val Val Ser Ser Ser Asn Gly Lys Lys Gly
 180 185 190
 Ile Cys Ser Ser Gly Ser Ala Ser Ser Leu Lys Gln Leu Ser Ser His
 195 200 205
 Ser Arg Asp His Asp Gln Ile Ser Val Gly Glu Ala Glu Val Ser Asp
 210 215 220
 Gln Asn Phe Val Asn Glu Gly Ile Lys Gly Glu Asn Gly Ser Ser Lys
 225 230 235 240
 Lys Met Lys Thr Val Met Met Ser Glu Ser Ser Ser Thr Asp Gln Val
 245 250 255
 Val Pro Leu Asn Lys Leu Leu Gln His Asp Val Asn Leu Lys Ser Val
 260 265 270

Ser

<210> 35
 <211> 738
 <212> DNA
 <213> Arabidopsis thaliana

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 aaagagtata tggaaacaga atggactaat gagaagcata gtttatatct taaatctatg 180
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 aatgggaaga agggaatatg cagctctggc tcagcctcta gtctcaagca gctaagctct 540
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 gttaacgaag gaataaaagg cgaaaacgga agctcgaaga agatgaagac ggtgatgatg 660
 agtgaatcgt cgagtaccga tcaggttggt ccaactcaata agctcttgca acatgacgta 720
 aatttgaagt ctgtttct 738

<210> 36
 <211> 246
 <212> PRT

2010-11-01 Substitute Sequence Listing

<213> Arabidopsis thaliana

<220>

<221> peptide

<222> (1)..(246)

<223> ceres Seq. ID no. 12323603

<400> 36

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Asp Ser Asp Asp Ser Ser Asp Asp Ala Ser Ser Val Glu Gly Glu Thr
          20          25          30
Thr Ser Ser Met Tyr Ser Ala Gly Lys Glu Tyr Met Glu Thr Glu Trp
          35          40          45
Thr Asn Glu Lys His Ser Leu Tyr Leu Lys Ser Met Glu Ala Ser Phe
          50          55          60
Val Asp Gln Leu Tyr Asn Ser Leu Gly Ala Leu Gly Lys Asn Glu Asn
 65          70          75          80
Val Ser Glu Ser Thr Arg Phe Gly Ser Gly Arg Lys Pro Ser Gln Glu
          85          90          95
Gln Phe Lys Val Leu His Asp Gly Phe Trp Gln Lys Ile Asn Val Lys
          100          105          110
Gln Pro Glu His Arg Ile Asn Gly Arg His Gly Gly Asn Ser His Glu
          115          120          125
Phe Leu Arg Ser Pro Trp Ile Lys His Tyr Lys Pro Leu Val Lys Thr
          130          135          140
Gln Ile Pro Val Thr Asp Glu Pro Glu Asn Gln Val Val Ser Ser Ser
          145          150          155          160
Asn Gly Lys Lys Gly Ile Cys Ser Ser Gly Ser Ala Ser Ser Leu Lys
          165          170          175
Gln Leu Ser Ser His Ser Arg Asp His Asp Gln Ile Ser Val Gly Glu
          180          185          190
Ala Glu Val Ser Asp Gln Asn Phe Val Asn Glu Gly Ile Lys Gly Glu
          195          200          205
Asn Gly Ser Ser Lys Lys Met Lys Thr Val Met Met Ser Glu Ser Ser
          210          215          220
Ser Thr Asp Gln Val Val Pro Leu Asn Lys Leu Leu Gln His Asp Val
          225          230          235          240
Asn Leu Lys Ser Val Ser
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<210> 37

<211> 633

<212> DNA

<213> Arabidopsis thaliana

2010-11-01 Substitute Sequence Listing

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gaacagttca aggttcttca tgatggtttc tggcagaaga ttaatgtgaa acaacctgaa 240
catcggatta acggaaggca cggtggtaat tctcatgagt ttcttaggag tccatggatt 300
aagcattata aacctttagt aaagacacaa atccccggtaa cggatgagcc cgaaaatcaa 360
gttggttagca gctctaattg gaagaaggga atatgcagct ctggctcagc ctctagtctc 420
aagcagctaa gctctcattc gcgtgaccac gaccaaata gcgttgagga agcagaggta 480
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<210> 38
<211> 211
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> peptide
<222> (1)..(211)
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20 25 30
Leu Tyr Asn Ser Leu Gly Ala Leu Gly Lys Asn Glu Asn Val Ser Glu
35 40 45
Ser Thr Arg Phe Gly Ser Gly Arg Lys Pro Ser Gln Glu Gln Phe Lys
50 55 60
Val Leu His Asp Gly Phe Trp Gln Lys Ile Asn Val Lys Gln Pro Glu
65 70 75 80
His Arg Ile Asn Gly Arg His Gly Gly Asn Ser His Glu Phe Leu Arg
85 90 95
Ser Pro Trp Ile Lys His Tyr Lys Pro Leu Val Lys Thr Gln Ile Pro
100 105 110
Val Thr Asp Glu Pro Glu Asn Gln Val Val Ser Ser Ser Asn Gly Lys
115 120 125
Lys Gly Ile Cys Ser Ser Gly Ser Ala Ser Ser Leu Lys Gln Leu Ser
130 135 140
Ser His Ser Arg Asp His Asp Gln Ile Ser Val Gly Glu Ala Glu Val

[illegible]

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<210> 39
<211> 960
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(960)
<223> ceres Seq. ID no. 13491409
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| ccacaaagat | aagccaacaa | tggttggtga | ttacagagga | cgcttttagta | gccgtcgttt | | 120 |
| ctccgatgac | tctgacgatt | cttccgacga | tgcttcttcc | gtggagggag | agaccacttc | | 180 |
| ttccatgtac | tctgcgggga | aagagtatat | ggaaacagaa | tggactaatg | agaagcatag | | 240 |
| tttatatctt | aatcttatgg | aagcttcatt | cgtagatcag | ttatataact | cgctcggagc | | 300 |
| tctcgggaag | aacgagaatg | tatccgaatc | aacgaggttc | ggtagcggta | gaaaaccgtc | | 360 |
| tcaagaacag | ttcaaggttc | ttcatgatgg | tttctggcag | aagattaatg | tgaacaacc | | 420 |
| tgaacatcgg | attaacggaa | ggcacggtgg | taattctcat | gagtttctta | ggagtccatg | | 480 |
| gattaagcat | tataaacctt | tagtaaagac | acaaatcccg | gtaacggatg | agcccgaaaa | | 540 |
| tcaagttggt | agcagctcta | atgggaagaa | gggaatatgc | agctctggct | cagcctctag | | 600 |
| tctcaagcag | ctaagctctc | attcgcgtga | ccacgaccaa | atcagcgttg | gagaagcaga | | 660 |
| ggtatcggat | cagaactttg | ttaacgaagg | aataaaaggc | gaaaacggaa | gctcgaagaa | | 720 |
| gatgaagacg | gtgatgatga | gtgaatcgtc | gagtaccgat | caggttgttc | cactcaataa | | 780 |
| actcttgcaa | catgacgtaa | atttgaagtc | tgtttcttga | gaggtcagat | ggtgaagctt | | 840 |
| tatatgagga | gagaattttg | taatgtatat | atatttgcac | aacttataag | tcaaattttac | | 900 |
| tatccttagt | tacaagtttc | ttcatcatat | atccctaact | ataaatatat | ttatatgccc | | 960 |
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<210> 40

2010-11-01 Substitute Sequence Listing

<211> 816
<212> DNA
<213> Arabidopsis thaliana

<400> 40
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 caagaacagt tcaaggttct tcatgatggt ttctggcaga agattaatgt gaaacaacct 420
 gaacatcgga ttaacggaag gcacggtggt aattctcatg agtttcttag gagtccatgg 480
 attaagcatt ataaaccttt agtaaagaca caaatccccg taacggatga gcccgaataa 540
 caagttgta gcagctctaa tgggaagaag ggaatatgca gctctggctc agcctctagt 600
 ctcaagcagc taagctctca ttcgcgtgac caccacaaa tcagcgttgg agaagcagag 660
 gtatcggatc agaactttgt taacgaagga ataaaaggcg aaaacggaag ctcgaagaag 720
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 ctcttgcaac atgacgtaaa tttgaagtct gtttct 816

<210> 41
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<213> Arabidopsis thaliana

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<222> (1)..(272)
<223> ceres Seq. ID no. 13491410

<400> 41
 Phe Leu Phe Leu Ser Phe Ser Leu Ile Phe Phe Ile Phe Phe Phe Phe
 1 5 10 15
 Ser Leu Ser Leu His Lys Asp Lys Pro Thr Met Val Gly Asp Tyr Arg
 20 25 30
 Gly Arg Phe Ser Ser Arg Arg Phe Ser Asp Asp Ser Asp Asp Ser Ser
 35 40 45
 Asp Asp Ala Ser Ser Val Glu Gly Glu Thr Thr Ser Ser Met Tyr Ser
 50 55 60
 Ala Gly Lys Glu Tyr Met Glu Thr Glu Trp Thr Asn Glu Lys His Ser
 65 70 75 80
 Leu Tyr Leu Lys Ser Met Glu Ala Ser Phe Val Asp Gln Leu Tyr Asn
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85

90

95

Ser Leu Gly Ala Leu Gly Lys Asn Glu Asn Val Ser Glu Ser Thr Arg
100 105 110
Phe Gly Ser Gly Arg Lys Pro Ser Gln Glu Gln Phe Lys Val Leu His
115 120 125
Asp Gly Phe Trp Gln Lys Ile Asn Val Lys Gln Pro Glu His Arg Ile
130 135 140
Asn Gly Arg His Gly Gly Asn Ser His Glu Phe Leu Arg Ser Pro Trp
145 150 155 160
Ile Lys His Tyr Lys Pro Leu Val Lys Thr Gln Ile Pro Val Thr Asp
165 170 175
Glu Pro Glu Asn Gln Val Val Ser Ser Ser Asn Gly Lys Lys Gly Ile
180 185 190
Cys Ser Ser Gly Ser Ala Ser Ser Leu Lys Gln Leu Ser Ser His Ser
195 200 205
Arg Asp His Asp Gln Ile Ser Val Gly Glu Ala Glu Val Ser Asp Gln
210 215 220
Asn Phe Val Asn Glu Gly Ile Lys Gly Glu Asn Gly Ser Ser Lys Lys
225 230 235 240
Met Lys Thr Val Met Met Ser Glu Ser Ser Ser Thr Asp Gln Val Val
245 250 255
Pro Leu Asn Lys Leu Leu Gln His Asp Val Asn Leu Lys Ser Val Ser
260 265 270

<210> 42
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aaagagtata tggaaacaga atggactaat gagaagcata gtttatatct taaatctatg 180
gaagcttcat tcgtagatca gttatataac tcgctcggag ctctcgggaa gaacgagaat 240
gtatccgaat caacgagggt cggtagcgggt agaaaaccgt ctcaagaaca gttcaagggt 300
cttcatgatg gtttctggca gaagattaat gtgaaacaac ctgaacatcg gattaacgga 360
aggcacggtg gtaattctca tgagtttctt aggagtccat ggattaagca ttataaacct 420
ttagtaaaga cacaaatccc ggtaacggat gagccccgaaa atcaagttgt tagcagctct 480
aatgggaaga agggaaatag cagctctggc tcagcctcta gtctcaagca gctaagctct 540
cattcgcgtg accacgacca aatcagcgtt ggagaagcag aggtatcgga tcagaacttt 600
gttaacgaag gaataaaagg cgaaaacgga agctcgaaga agatgaagac ggtgatgatg 660

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agtgaatcgt cgagtaccga tcaggttggt ccactcaata aactcttgca acatgacgta 720
aatttgaagt ctgtttct 738

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Asp Ser Asp Asp Ser Ser Asp Asp Ala Ser Ser Val Glu Gly Glu Thr
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Thr Ser Ser Met Tyr Ser Ala Gly Lys Glu Tyr Met Glu Thr Glu Trp
35 40 45
Thr Asn Glu Lys His Ser Leu Tyr Leu Lys Ser Met Glu Ala Ser Phe
50 55 60
Val Asp Gln Leu Tyr Asn Ser Leu Gly Ala Leu Gly Lys Asn Glu Asn
65 70 75 80
Val Ser Glu Ser Thr Arg Phe Gly Ser Gly Arg Lys Pro Ser Gln Glu
85 90 95
Gln Phe Lys Val Leu His Asp Gly Phe Trp Gln Lys Ile Asn Val Lys
100 105 110
Gln Pro Glu His Arg Ile Asn Gly Arg His Gly Gly Asn Ser His Glu
115 120 125
Phe Leu Arg Ser Pro Trp Ile Lys His Tyr Lys Pro Leu Val Lys Thr
130 135 140
Gln Ile Pro Val Thr Asp Glu Pro Glu Asn Gln Val Val Ser Ser Ser
145 150 155 160
Asn Gly Lys Lys Gly Ile Cys Ser Ser Gly Ser Ala Ser Ser Leu Lys
165 170 175
Gln Leu Ser Ser His Ser Arg Asp His Asp Gln Ile Ser Val Gly Glu
180 185 190
Ala Glu Val Ser Asp Gln Asn Phe Val Asn Glu Gly Ile Lys Gly Glu
195 200 205
Asn Gly Ser Ser Lys Lys Met Lys Thr Val Met Met Ser Glu Ser Ser
210 215 220
Ser Thr Asp Gln Val Val Pro Leu Asn Lys Leu Leu Gln His Asp Val
225 230 235 240

2010-11-01 Substitute Sequence Listing

Asn Leu Lys Ser Val Ser
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gggaagaacg agaatgtatc cgaatcaacg aggttcggta gcggtagaaa accgtctcaa 180
gaacagttca aggttcttca tgatggtttc tggcagaaga ttaatgtgaa acaacctgaa 240
catcggatta acggaaggca cggtggtaat tctcatgagt ttcttaggag tccatggatt 300
aagcattata aacctttagt aaagacacaa atccccgtaa cggatgagcc cgaaaatcaa 360
gttgtagca gctctaattg gaagaaggga atatgcagct ctggctcagc ctctagtctc 420
aagcagctaa gctctcattc gcgtgaccac gaccaaata gcgttgagga agcagaggta 480
tcggatcaga actttgttaa cgaaggaata aaaggcgaaa acggaagctc gaagaagatg 540
aagacggtga tgatgagtga atcgtcgagt accgatcagg ttgttccact caataaactc 600
ttgcaacatg acgtaaaattt gaagtctggt tct 633

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Lys His Ser Leu Tyr Leu Lys Ser Met Glu Ala Ser Phe Val Asp Gln
20 25 30
Leu Tyr Asn Ser Leu Gly Ala Leu Gly Lys Asn Glu Asn Val Ser Glu
35 40 45
Ser Thr Arg Phe Gly Ser Gly Arg Lys Pro Ser Gln Glu Gln Phe Lys
50 55 60
Val Leu His Asp Gly Phe Trp Gln Lys Ile Asn Val Lys Gln Pro Glu
65 70 75 80
His Arg Ile Asn Gly Arg His Gly Gly Asn Ser His Glu Phe Leu Arg
85 90 95
Ser Pro Trp Ile Lys His Tyr Lys Pro Leu Val Lys Thr Gln Ile Pro
100 105 110

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Val Thr Asp Glu Pro Glu Asn Gln Val Val Ser Ser Ser Asn Gly Lys
115 120 125
Lys Gly Ile Cys Ser Ser Gly Ser Ala Ser Ser Leu Lys Gln Leu Ser
130 135 140
Ser His Ser Arg Asp His Asp Gln Ile Ser Val Gly Glu Ala Glu Val
145 150 155 160
Ser Asp Gln Asn Phe Val Asn Glu Gly Ile Lys Gly Glu Asn Gly Ser
165 170 175
Ser Lys Lys Met Lys Thr Val Met Met Ser Glu Ser Ser Ser Thr Asp
180 185 190
Gln Val Val Pro Leu Asn Lys Leu Leu Gln His Asp Val Asn Leu Lys
195 200 205
Ser Val Ser
210

<210> 46
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<213> Artificial Sequence

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cgcatctcta attcatcttc gtcgagagga gctgttcctc ttctttgccg cctcgaatct 180
gggactggtc ggttttcttg atccctgctg cctgtcgggt tctcgagagg tgtaaaatcc 240
aatggagggt gtgtcatcgt tgaaccagcc gttgatcaac gacgaccggc agcccgtgcc 300
cagcagtatc gccaaagggtg atcaaatcca aggcctgttg tcgggtgaat ggacaaatga 360
gcggcacagc tcgtacataa gctccatgga ggcattcttc gtggagcaac tccgtagtgg 420
ttccaaggcc atccaggagg gcttgtgcca gagcatgagg attccgaggg atgatgctcg 480
cagccatgac gtccctgaga gtccgtgggt ggtggtgagg cgtttcaggc caccggtgtg 540
ccaccatggc gatggaatgg aagtggaacc ttgggtcgat ggttatggat caggtactga 600
cacggcccng agagaagggtc cggaccacg caagatagcg aaggcttctg ctattattga 660
agtcacggac cagaattttc ctgaggagg gattcaatcc agtaacggtg catgcaagag 720

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acagaaatct actcctggca atgcatcaaa tggccagggt acttaacaag atagtggaag 780
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gtactacgtg atgacaggtc gtgctgcagc tgcaagtagt ttggcttacc aaaatatgat 900
atcgtcgtcc tttctgcggt gtggagagta gaatatgcat atccacatct gcagagagca 960
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<210> 47
<211> 174
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<213> Artificial Sequence

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<223> clone peptide 486033

<220>
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<223> Xaa can be any naturally occurring amino acid

<400> 47

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Gln Pro Val Pro Ser Ser Ile Ala Lys Gly Asp Gln Ile Gln Gly Leu
20 25 30

Leu Ser Gly Glu Trp Thr Asn Glu Arg His Ser Ser Tyr Ile Ser Ser
35 40 45

Met Glu Ala Ser Phe Val Glu Gln Leu Arg Ser Gly Ser Lys Ala Ile
50 55 60

Gln Glu Gly Leu Cys Gln Ser Met Arg Ile Pro Arg Asp Asp Ala Arg
65 70 75 80

Ser His Asp Val Pro Glu Ser Pro Trp Val Val Val Arg Arg Phe Arg
85 90 95

Pro Arg Gly Val His His Gly Asp Gly Met Glu Val Glu Pro Leu Val
100 105 110

Asp Gly Tyr Gly Ser Gly Thr Asp Thr Ala Xaa Arg Glu Gly Pro Asp
115 120 125

Pro Arg Lys Ile Ala Lys Ala Ser Ala Ile Ile Glu Val Thr Asp Gln
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130

Asn Phe Pro Glu Glu Gly Ile Gln Ser Ser Asn Gly Ala Cys Lys Arg
145 150 155 160

Gln Lys Ser Thr Pro Gly Asn Ala Ser Asn Gly Gln Gly Thr
165 170

<210> 48
<211> 210
<212> PRT
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<220>
<223> Consensus sequence derived from various organisms

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serine or threonine

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<222> (5)..(5)
<223> Xaa is Thr or Pro

<220>
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<222> (7)..(8)
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serine or threonine

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<222> (9)..(9)
<223> Xaa is Met or Gly

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa is Tyr or Ile

<220>
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<222> (11)..(11)
<223> Xaa is a tiny amino acid, specifically, alanine, glycine,
serine or threonine

<220>
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<222> (12)..(12)
<223> Xaa is Ala or Lys

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<220>
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 <222> (14)..(14)
 <223> Xaa is Lys or Asn

 <220>
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 <222> (15)..(15)
 <223> Xaa is Glu or Arg

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 <221> misc_feature
 <222> (16)..(16)
 <223> Xaa is Tyr or Val

 <220>
 <221> misc_feature
 <222> (17)..(17)
 <223> Xaa is an aliphatic residue, specifically, isoleucine, valine,
 leucine, or methionine

 <220>
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 <222> (18)..(18)
 <223> Xaa is any amino acid

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 <222> (19)..(19)
 <223> Xaa is a tiny amino acid, specifically, alanine, glycine,
 serine or threonine

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 <223> At least 1 but as many as 4 of the Xaa amino acids can be present;
 Xaa is any amino acid

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 <222> (26)..(26)
 <223> Xaa is Asn or Asp

 <220>
 <221> misc_feature
 <222> (28)..(28)
 <223> Xaa is a positively charged residue, specifically, lysine, arginine,
 or histidine

 <220>
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 <223> Xaa is any amino acid

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 <223> Xaa is an aliphatic residue, specifically, isoleucine, valine,

2010-11-01 Substitute Sequence Listing
leucine, or methionine

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<222> (34)..(34)
<223> Xaa is Lys or Ser

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<222> (42)..(42)
<223> Xaa is any negatively charged amino acid, specifically,
aspartic acid or glutamic acid

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<222> (45)..(74)
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absent; Xaa is any amino acid

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<223> Xaa is an aliphatic residue, specifically, isoleucine, valine,
leucine, or methionine

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<222> (81)..(82)
<223> Xaa is any amino acid

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<222> (83)..(83)
<223> Xaa is Gln or Glu

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present; Xaa is any amino acid

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<223> Xaa is His or Cys

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 <220>
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 <223> Xaa is Leu or Pro

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 <223> Xaa is Ser or Asn

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 <223> Xaa is a positively charged residue, specifically, lysine, arginine, or histidine

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 <223> Xaa is a positively charged residue, specifically, lysine, arginine, or histidine

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 <222> (119)..(126)
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<221> misc_feature
<222> (131)..(131)
<223> Xaa is Glu or Asn

<220>
<221> misc_feature
<222> (132)..(139)
<223> Xaa is any amino acid

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or absent; Xaa is any amino acid

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serine or threonine

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serine or threonine

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<222> (154)..(154)

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 <223> Xaa is Gln or Lys

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 <222> (173)..(173)
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<220>
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<220>
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<220>
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 <222> (192)..(192)
 <223> Xaa is Ile or Ala

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        serine or threonine

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<223> Xaa is Asn or Thr

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<222> (197)..(197)
<223> Xaa is Gly or Glu

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        serine or threonine

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<221> misc_feature
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<223> Xaa is Met or Arg

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<220>

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<222> (210)..(210)

<223> Xaa is a tiny amino acid, specifically, alanine, glycine, serine or threonine

<400> 48

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Thr Xaa Glu Xaa His Xaa Xaa Tyr
20 25 30

Xaa Xaa Ser Met Glu Ala Ser Phe Val Xaa Gln Leu Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Trp Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp
115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Glu Val Xaa Asp Gln Asn Phe Xaa Xaa Xaa Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Lys Xaa Xaa Xaa Xaa Ser
195 200 205

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Xaa Xaa
210

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<211> 241
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<220>
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<223> Xaa is a tiny amino acid, specifically, alanine, glycine, serine or threonine

<220>
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<222> (3)..(10)
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<220>
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Xaa is any amino acid

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<220>
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Xaa is any amino acid

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<222> (34)..(34)
<223> Xaa is Asn or Asp

<220>
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<222> (36)..(36)
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or histidine

<220>

<221> misc_feature

<222> (38)..(39)

<223> Xaa is any amino acid

<220>

<221> misc_feature

<222> (41)..(41)

<223> Xaa is an aliphatic residue, specifically, isoleucine, valine, leucine, or methionine

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<222> (42)..(42)

<223> Xaa is any amino acid

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<222> (43)..(43)

<223> Xaa is Ser or Tyr

<220>

<221> misc_feature

<222> (44)..(44)

<223> Xaa is an aliphatic residue, specifically, isoleucine, valine, leucine, or methionine

<220>

<221> misc_feature

<222> (46)..(46)

<223> Xaa is a tiny amino acid, specifically, alanine, glycine, serine or threonine

<220>

<221> misc_feature

<222> (50)..(50)

<223> Xaa is any amino acid

<220>

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<222> (52)..(52)

<223> Xaa is Lys or Ser

<220>

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<222> (53)..(135)

<223> At least 8 but as many as 83 of the Xaa amino acids can be present; Xaa is any amino acid

<220>

<221> misc_feature

<222> (136)..(136)

<223> Xaa is Pro or Glu

<220>

<221> misc_feature

<222> (137)..(137)

<223> Xaa is any aromatic residue, specifically, phenylalanine, tyrosine, and tryptophan

<220>

2010-11-01 Substitute Sequence Listing

85

90

95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Gln Asn Phe Xaa Xaa
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Xaa

<210> 50

<211> 19

<212> DNA

<213> Artificial sequence

<220>

<223> oligo primer used in the generation of labeled probes for hybridization from first-strand cDNA

<400> 50

tttttttttt ttttttttv

19